

160754

Schreiber, David

From: Steadman, David (AU1652)
Sent: Tuesday, July 12, 2005 12:29 PM
To: Schreiber, David
Subject: 10/600,751 sequence search request

NAME: David Steadman
AU: 1656
Date: 07/12/05
Office: Remsen 2B05
Mailbox: Remsen 3C70

Please perform the following search or searches in commercial and interference databases:

- 1) Standard search of SEQ ID NO:6 against amino acid databases.
- 2) Standard search of SEQ ID NO:9 against amino acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
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Phone: (571) 272-0942

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:06:28 ; Search time 223.808 Seconds
(without alignments)
444.119 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE.....TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1340	100.0	257	8 ADH26660	Adh26660 Human wil
2	1340	100.0	777	1 AAP80919	Aap80919 Sequence
3	1340	100.0	777	2 AAY21623	Aay21623 Ligand bi
4	1340	100.0	777	6 ABU08023	Abu08023 Wild-type
5	1340	100.0	777	6 ABR44285	Abr44285 Human GRa
6	1340	100.0	777	7 ADE57452	Ade57452 Human Pro
7	1340	100.0	777	7 ADF30368	Adf30368 Human ful
8	1340	100.0	777	7 ADG10636	Adg10636 Human STA
9	1340	100.0	777	7 ADF73070	Adf73070 Glucocort
10	1340	100.0	777	8 ADH26656	Adh26656 Human wil
11	1340	100.0	777	8 ADH67937	Adh67937 Human glu
12	1340	100.0	777	8 ADP05673	Adp05673 Human nuc
13	1340	100.0	777	8 ADS88247	Ads88247 Human pro
14	1340	100.0	777	8 ADQ39890	Adq39890 Human myo
15	1340	100.0	777	8 ADQ39891	Adq39891 Human myo
16	1340	100.0	781	6 ABR41246	Abr41246 Human DIT
17	1340	100.0	1003	6 ABP58320	Abp58320 Glucocort
18	1338	99.9	257	6 ABU08045	Abu08045 Mutant hu
19	1336	99.7	257	6 ABU08044	Abu08044 Mutant hu
20	1335	99.6	257	6 ABU08043	Abu08043 Mutant hu
21	1335	99.6	667	2 AAW44701	Aaw44701 Chimeric
22	1335	99.6	777	2 AAW44700	Aaw44700 Mutant nu
23	1333	99.5	257	6 ABU08042	Abu08042 Mutant hu
24	1332	99.4	257	8 ADH26662	Adh26662 Human mut

25	1332	99.4	777	6	ABU08024	Abu08024	Mutant	hu
26	1332	99.4	777	8	ADH26658	Adh26658	Human	mut
27	1331	99.3	257	6	ABU08049	Abu08049	Mutant	hu
28	1331	99.3	777	6	ABU08025	Abu08025	Mutant	hu
29	1330	99.3	257	6	ABU08046	Abu08046	Mutant	hu
30	1329	99.2	255	8	ADI29487	Adi29487	Human	lig
31	1329	99.2	483	6	ABP58319	Abp58319	Glucocort	
32	1328	99.1	777	7	ADF73072	Adf73072	Glucocort	
33	1327	99.0	257	6	ABU08047	Abu08047	Mutant	hu
34	1327	99.0	257	6	ABU08048	Abu08048	Mutant	hu
35	1326	99.0	257	6	ABU08041	Abu08041	Mutant	hu
36	1323	98.7	276	7	ADF30365	Adf30365	Human	glu
37	1320	98.5	277	7	ADF30366	Adf30366	Human	glu
38	1318	98.4	613	4	AAB47153	Aab47153	iCre-FRT-	
39	1308	97.6	797	7	ADF73074	Adf73074	Glucocort	
40	1304	97.3	251	3	AAB26787	Aab26787	Glucocort	
41	1291	96.3	739	8	ADH67939	Adh67939	Mouse	glu
42	1291	96.3	783	8	ADH67952	Adh67952	Mouse	glu
43	1291	96.3	783	8	ADP05675	Adp05675	Mouse	nuc
44	1284	95.8	284	3	AAB19249	Aab19249	A rat	glu
45	1284	95.8	795	7	ADE57450	Ade57450	Rat	Prote

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:09:14 ; Search time 56.9004 Seconds
(without alignments)
337.165 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE.....TNQIPKYSNGNIKLLFHQK 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1340	100.0	777	3	US-08-764-870-13	Sequence 13, Appl
2	1340	100.0	777	3	US-08-980-115-13	Sequence 13, Appl
3	1335	99.6	667	4	US-09-125-491C-4	Sequence 4, Appli
4	1335	99.6	777	4	US-09-125-491C-2	Sequence 2, Appli
5	1291.5	96.4	356	6	5223606-7	Patent No. 5223606
6	1291.5	96.4	356	6	5223606-7	Patent No. 5223606
7	1284	95.8	284	2	US-08-592-214A-24	Sequence 24, Appl
8	1284	95.8	284	3	US-09-149-976-24	Sequence 24, Appl
9	1284	95.8	795	1	US-07-716-827C-5	Sequence 5, Appli
10	1276	95.2	284	3	US-08-659-188-20	Sequence 20, Appl
11	1276	95.2	284	3	US-08-655-227-20	Sequence 20, Appl
12	1276	95.2	284	3	US-08-655-241-20	Sequence 20, Appl
13	1276	95.2	284	3	US-09-398-326-20	Sequence 20, Appl
14	1276	95.2	284	4	US-09-853-450-20	Sequence 20, Appl
15	1272	94.9	1070	4	US-09-091-042A-2	Sequence 2, Appli
16	1254	93.6	534	3	US-08-875-223-8	Sequence 8, Appli
17	773	57.7	984	3	US-08-764-870-15	Sequence 15, Appl
18	773	57.7	984	3	US-08-980-115-15	Sequence 15, Appl
19	773	57.7	984	4	US-09-976-594-127	Sequence 127, App
20	731.5	54.6	363	6	5223606-6	Patent No. 5223606
21	731.5	54.6	363	6	5223606-6	Patent No. 5223606
22	729.5	54.4	933	3	US-08-764-870-14	Sequence 14, Appl
23	729.5	54.4	933	3	US-08-980-115-14	Sequence 14, Appl
24	729.5	54.4	990	4	US-09-949-016-10562	Sequence 10562, A
25	724.5	54.1	255	4	US-09-687-609A-2	Sequence 2, Appli
26	662.5	49.4	260	4	US-09-687-609A-1	Sequence 1, Appli

27	662.5	49.4	452	3	US-08-764-870-16	Sequence 16, Appl
28	662.5	49.4	452	3	US-08-980-115-16	Sequence 16, Appl
29	662.5	49.4	918	3	US-09-041-886-11	Sequence 11, Appl
30	662.5	49.4	919	4	US-09-538-092-895	Sequence 895, App
31	662.5	49.4	923	4	US-09-497-822C-19	Sequence 19, Appl
32	643.5	48.0	996	4	US-09-497-822C-21	Sequence 21, Appl
33	512	38.2	98	4	US-09-652-345-4	Sequence 4, Appli
34	341	25.4	98	4	US-09-652-345-3	Sequence 3, Appli
35	323	24.1	60	5	PCT-US94-14074-1	Sequence 1, Appli
36	240.5	17.9	596	2	US-08-836-620A-16	Sequence 16, Appl
37	238	17.8	264	4	US-09-660-979-1	Sequence 1, Appli
38	236.5	17.6	595	4	US-10-052-092-30	Sequence 30, Appl
39	235.5	17.6	701	4	US-10-052-092-12	Sequence 12, Appl
40	235	17.5	595	3	US-08-764-870-12	Sequence 12, Appl
41	235	17.5	595	3	US-08-980-115-12	Sequence 12, Appl
42	233.5	17.4	595	4	US-10-052-092-31	Sequence 31, Appl
43	233	17.4	547	4	US-10-052-092-10	Sequence 10, Appl
44	233	17.4	591	2	US-08-836-620A-17	Sequence 17, Appl
45	233	17.4	595	3	US-09-041-886-35	Sequence 35, Appl

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:16:10 ; Search time 204.841 Seconds
(without alignments)
484.703 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE.....TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1340	100.0	777	9	US-09-308-295-4	Sequence 4, Appli
2	1340	100.0	777	14	US-10-153-668-226	Sequence 226, App
3	1340	100.0	777	16	US-10-661-217-2	Sequence 2, Appli
4	1340	100.0	777	16	US-10-661-217-4	Sequence 4, Appli
5	1340	100.0	777	17	US-10-741-600-1553	Sequence 1553, Ap
6	1340	100.0	777	17	US-10-741-600-1554	Sequence 1554, Ap
7	1340	100.0	1003	14	US-10-151-133-2	Sequence 2, Appli
8	1329	99.2	483	14	US-10-151-133-1	Sequence 1, Appli
9	1276	95.2	284	9	US-09-853-450-20	Sequence 20, Appl
10	1276	95.2	284	16	US-10-794-923-20	Sequence 20, Appl

11	1272	94.9	1070	14	US-10-001-486B-2	Sequence 2, Appli
12	1081	80.7	742	9	US-09-308-295-2	Sequence 2, Appli
13	1081	80.7	742	16	US-10-755-889-550	Sequence 550, App
14	773	57.7	984	15	US-10-087-080-36	Sequence 36, Appl
15	729.5	54.4	258	14	US-10-220-981-3	Sequence 3, Appli
16	729.5	54.4	314	9	US-09-887-280-4	Sequence 4, Appli
17	729.5	54.4	381	16	US-10-416-708A-56	Sequence 56, Appl
18	729.5	54.4	933	14	US-10-207-655-63	Sequence 63, Appl
19	729.5	54.4	933	15	US-10-332-176A-4	Sequence 4, Appli
20	724.5	54.1	251	16	US-10-469-866-16	Sequence 16, Appl
21	724.5	54.1	255	16	US-10-878-851-2	Sequence 2, Appli
22	695.5	51.9	240	9	US-09-905-176-13	Sequence 13, Appl
23	684.5	51.1	630	15	US-10-400-053-15	Sequence 15, Appl
24	684.5	51.1	654	15	US-10-400-053-14	Sequence 14, Appl
25	682.5	50.9	630	15	US-10-400-053-24	Sequence 24, Appl
26	678.5	50.6	574	15	US-10-332-176A-6	Sequence 6, Appli
27	678.5	50.6	574	15	US-10-332-176A-8	Sequence 8, Appli
28	678.5	50.6	599	15	US-10-332-176A-10	Sequence 10, Appl
29	669.5	50.0	689	14	US-10-202-846-2	Sequence 2, Appli
30	662.5	49.4	260	16	US-10-878-851-1	Sequence 1, Appli
31	662.5	49.4	263	14	US-10-220-981-1	Sequence 1, Appli
32	662.5	49.4	388	9	US-09-997-267-2	Sequence 2, Appli
33	662.5	49.4	895	16	US-10-476-724A-2	Sequence 2, Appli
34	662.5	49.4	895	16	US-10-476-724A-4	Sequence 4, Appli
35	662.5	49.4	899	16	US-10-484-950-4	Sequence 4, Appli
36	662.5	49.4	899	16	US-10-484-950-6	Sequence 6, Appli
37	662.5	49.4	899	16	US-10-484-950-8	Sequence 8, Appli
38	662.5	49.4	902	17	US-10-886-384-21	Sequence 21, Appl
39	662.5	49.4	907	13	US-10-008-739A-2	Sequence 2, Appli
40	662.5	49.4	918	15	US-10-375-592A-3	Sequence 3, Appli
41	662.5	49.4	919	14	US-10-205-823-36	Sequence 36, Appl
42	662.5	49.4	919	15	US-10-058-270A-94	Sequence 94, Appl
43	662.5	49.4	919	16	US-10-333-894A-21	Sequence 21, Appl
44	662.5	49.4	923	17	US-10-886-384-19	Sequence 19, Appl
45	654.5	48.8	906	15	US-10-375-592A-4	Sequence 4, Appli

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:08:54 ; Search time 45.5203 Seconds
(without alignments)
543.224 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE.....TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1340	100.0	777	1 QRHUGA	glucocorticoid rec
2	1291	96.3	783	1 A25691	glucocorticoid rec
3	1284	95.8	795	1 QRRTG	glucocorticoid rec
4	1233	92.0	771	2 A54273	glucocorticoid rec
5	1081	80.7	742	1 QRHUGB	glucocorticoid rec
6	1072	80.0	776	1 S44047	glucocorticoid rec
7	1011	75.4	758	2 S60586	glucocorticoid rec
8	773	57.7	984	2 A29513	mineralocorticoid
9	762	56.9	981	2 A41401	mineralocorticoid
10	732.5	54.7	923	2 A39596	progesterone recep
11	731.5	54.6	930	2 A25923	progesterone recep
12	729.5	54.4	933	1 QRHUP	progesterone recep
13	727.5	54.3	923	2 I53280	progesterone recep
14	723.5	54.0	786	2 A35466	progesterone recep
15	662.5	49.4	899	2 A35895	androgen receptor
16	662.5	49.4	902	2 B40494	androgen receptor
17	662.5	49.4	919	2 A39248	androgen receptor
18	654.5	48.8	910	2 A34721	androgen receptor
19	631.5	47.1	344	2 I51330	androgen receptor
20	623	46.5	911	2 B34721	androgen receptor
21	612.5	45.7	848	2 JG0194	androgen receptor
22	291.5	21.8	110	2 I53287	progesterone recep
23	240.5	17.9	600	1 QRRTE	estrogen receptor
24	239.5	17.9	599	1 QRMSE	estrogen receptor
25	235.5	17.6	701	2 S64737	80K estrogen recep
26	233.5	17.4	595	2 I47140	estradiol receptor
27	233	17.4	595	1 QRHUE	estrogen receptor
28	230.5	17.2	166	2 S35795	androgen receptor

29	230.5	17.2	589	1	QRCHE	estrogen receptor
30	227.5	17.0	433	2	B29345	steroid hormone re
31	221.5	16.5	521	2	A29345	steroid hormone re
32	215.5	16.1	433	2	S58087	estrogen receptor
33	214.5	16.0	477	2	S71400	estrogen receptor
34	214.5	16.0	530	2	JC5939	estrogen receptor
35	214	16.0	586	1	QRXLE	estrogen receptor
36	207.5	15.5	503	2	JW0046	estrogen receptor
37	188.5	14.1	620	2	T10423	estrogen receptor
38	187	14.0	535	2	S58224	oestrogen receptor
39	177	13.2	462	2	S44490	RXR type hormone r
40	173.5	12.9	574	2	A37197	estrogen receptor
41	165.5	12.4	536	2	A56590	ecdysteroid recept
42	145.5	10.9	878	2	A41055	ecdysone receptor
43	144.5	10.8	808	1	S33708	nuclear steroid/th
44	135	10.1	385	2	I53158	orphan nuclear rec
45	135	10.1	441	2	I50515	retinoid X recepto

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:07:23 ; Search time 212.428 Seconds
(without alignments)
619.524 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEIV.....TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1340	100.0	777	1	GCR_HUMAN	P04150 homo sapien
2	1340	100.0	777	2	Q6N0A4	Q6n0a4 homo sapien
3	1329	99.2	777	1	GCR_AOTNA	P79686 aotus nancy
4	1329	99.2	777	1	GCR_SAIBB	O13186 saimiri bol
5	1329	99.2	777	2	Q6XLJ0	Q6xlj0 callithrix
6	1329	99.2	778	1	GCR_SAISC	O46567 saimiri sci
7	1326	99.0	777	1	GCR_SAGOE	P79269 saguinus oe
8	1298	96.9	583	2	Q865Y6	Q865y6 bos taurus
9	1291	96.3	783	1	GCR_MOUSE	P06537 mus musculu
10	1289	96.2	772	1	GCR_RABIT	P59667 oryctolagus
11	1284	95.8	795	1	GCR_RAT	P06536 rattus norv
12	1268	94.6	776	1	GCR_TUPGB	Q95267 tupaia glis
13	1233	92.0	771	1	GCR_CAVPO	P49115 cavia porce
14	1149	85.7	711	1	GCR_PIG	Q9nlu3 sus scrofa
15	1072	80.0	776	1	GCR_XENLA	P49844 xenopus lae
16	1072	80.0	776	2	Q6DDL0	Q6ddl0 xenopus lae
17	1034	77.2	669	2	Q6RKQ3	Q6rkq3 oncorhynch
18	1025	76.5	793	2	Q8JJ91	Q8jj91 haplochromi
19	1025	76.5	802	2	Q8JJ90	Q8jj90 haplochromi
20	1024	76.4	807	1	GCR_PAROL	O73673 paralichthy
21	1022	76.3	779	2	Q8JJ92	Q8jj92 haplochromi
22	1019	76.0	818	2	Q6QB13	Q6qb13 dicentrarch
23	1011	75.4	758	1	GCR_ONCMY	P49843 oncorhynch
24	794.5	59.3	779	2	Q6IVJ3	Q6ivj3 dicentrarch
25	773	57.7	984	1	MCR_HUMAN	P08235 homo sapien
26	769	57.4	982	1	MCR_SAISC	Q9n0w8 saimiri sci
27	769	57.4	983	2	Q6XLI9	Q6xli9 callithrix
28	769	57.4	987	2	Q6XLI8	Q6xli8 callithrix
29	762	56.9	981	1	MCR_RAT	P22199 rattus norv
30	761	56.8	978	1	MCR_MOUSE	Q8vii8 mus musculu

31	753.5	56.2	612	1	MCR_XENLA	Q91573	xenopus lae
32	753.5	56.2	979	2	Q66J29	Q66j29	xenopus lae
33	740.5	55.3	993	2	Q8JJ89	Q8jj89	haplochromi
34	738	55.1	977	1	MCR_TUPGB	Q29131	tupaia glis
35	736.5	55.0	583	2	Q9DEV4	Q9dev4	xenopus lae
36	736.5	55.0	703	2	Q8UVY3	Q8uvy3	xenopus lae
37	735.5	54.9	732	2	Q9DDU9	Q9ddu9	xenopus lae
38	732.5	54.7	698	2	Q8BW69	Q8bw69	mus musculu
39	732.5	54.7	923	1	PRGR_MOUSE	Q00175	mus musculu
40	731.5	54.6	482	2	Q690N0	Q690n0	bos taurus
41	731.5	54.6	930	1	PRGR_RABIT	P06186	oryctolagus
42	730.5	54.5	939	1	PRGR_CANFA	Q9glw0	canis famil
43	729.5	54.4	933	1	PRGR_HUMAN	P06401	homo sapien
44	727.5	54.3	923	1	PRGR_RAT	Q63449	rattus norv
45	723.5	54.0	786	1	PRGR_CHICK	P07812	gallus gall

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:06:28 ; Search time 12.1919 Seconds
(without alignments)
444.119 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	71	100.0	14	8	ADH26663	Adh26663 Human TIF
2	71	100.0	19	5	AAU86409	Aau86409 Oestrogen
3	71	100.0	19	8	ADM79120	Adm79120 Oestrogen
4	71	100.0	20	7	ADG17808	Adg17808 Binding a
5	71	100.0	20	8	ADJ92851	Adj92851 Co-activa
6	71	100.0	25	3	AAJ99871	Aaj99871 Human nuc
7	71	100.0	25	3	AAB13527	Aab13527 Farnesoid
8	71	100.0	25	4	AAE12667	Aae12667 Biotinyla
9	71	100.0	25	5	AAU84221	Aau84221 Molecular
10	71	100.0	25	6	ABU08031	Abu08031 Nuclear r
11	71	100.0	31	3	AAJ58284	Aaj58284 Human p16
12	71	100.0	31	3	AAJ58290	Aaj58290 Human p16
13	71	100.0	31	3	AAJ58287	Aaj58287 Human p16
14	71	100.0	31	5	AAO20842	Aao20842 p160 coac
15	71	100.0	31	5	AAO20840	Aao20840 p160 coac
16	71	100.0	31	5	AAO20841	Aao20841 p160 coac
17	71	100.0	133	5	AAE16444	Aae16444 GRIP pept
18	71	100.0	248	8	ADM93125	Adm93125 Human lig
19	71	100.0	730	8	ADM93130	Adm93130 Human fus
20	71	100.0	1263	6	AAE36002	Aae36002 Human TIF
21	71	100.0	1263	6	ABR43917	Abr43917 Human TIF
22	71	100.0	1263	8	ADN12166	Adn12166 Human TIF
23	71	100.0	1464	2	AAW42632	Aaw42632 Human tra
24	71	100.0	1464	5	ABG69021	Abg69021 Human ste

25	71	100.0	1464	5	AAE22565	Aae22565 Human ste
26	71	100.0	1464	8	ADM93126	Adm93126 Human tra
27	71	100.0	1464	8	ADQ95898	Adq95898 T cell ac
28	63	88.7	1463	2	AAW99482	Aaw99482 Murine NC
29	61	85.9	20	7	ADG17850	Adg17850 Binding a
30	59	83.1	20	7	ADG17811	Adg17811 Binding a
31	59	83.1	20	8	ADJ92854	Adj92854 Co-activa
32	59	83.1	22	4	AAE13047	Aae13047 Nuclear c
33	59	83.1	25	3	AAy99870	Aay99870 Human nuc
34	59	83.1	25	3	AAB13526	Aab13526 Farnesoid
35	59	83.1	25	4	AAE12666	Aae12666 Biotinyla
36	59	83.1	25	5	AAU84220	Aau84220 Molecular
37	59	83.1	32	3	AAy58296	Aay58296 Human pl6
38	59	83.1	32	3	AAy58299	Aay58299 Human pl6
39	59	83.1	32	3	AAy58293	Aay58293 Human pl6
40	59	83.1	32	5	AAO20845	Aao20845 pl60 coac
41	59	83.1	32	5	AAO20844	Aao20844 pl60 coac
42	59	83.1	32	5	AAO20843	Aao20843 pl60 coac
43	59	83.1	149	4	AAM17609	Aam17609 Peptide #
44	59	83.1	149	4	ABB36630	Abb36630 Peptide #
45	59	83.1	149	4	AAM30127	Aam30127 Peptide #

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:09:14 ; Search time 3.09963 Seconds
(without alignments)
337.165 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	71	100.0	25	4	US-09-868-397-3
2	71	100.0	1463	4	US-09-445-353E-3
3	71	100.0	1463	4	US-09-949-016-11696
4	71	100.0	1464	3	US-08-891-640-2
5	71	100.0	1464	4	US-09-949-016-6738
6	59	83.1	25	4	US-09-868-397-2
7	59	83.1	951	4	US-09-125-635-8
8	59	83.1	1302	4	US-09-949-016-10852
9	59	83.1	1402	4	US-09-125-635-12
10	59	83.1	1402	4	US-09-445-353E-2
11	59	83.1	1420	4	US-09-125-635-4
12	58	81.7	48	3	US-08-891-640-5
13	54	76.1	14	3	US-09-302-305C-4
14	54	76.1	14	3	US-09-302-305C-17
15	54	76.1	15	4	US-09-445-353E-6
16	54	76.1	1036	3	US-08-891-640-3
17	54	76.1	1061	3	US-08-701-154A-5
18	54	76.1	1076	4	US-09-949-016-7421
19	45	63.4	9	4	US-09-053-611-6
20	45	63.4	9	4	US-08-975-614-8
21	45	63.4	10	4	US-08-975-614-9
22	45	63.4	11	4	US-08-975-614-10
23	44	62.0	388	3	US-09-134-001C-4951
24	41	57.7	663	4	US-09-107-532A-6861
25	40	56.3	295	4	US-09-248-796A-17141
26	39	54.9	8	3	US-09-419-826-39

27	39	54.9	8	4	US-08-975-614-3	Sequence 3, Appli
28	39	54.9	219	4	US-09-614-912-182	Sequence 182, App
29	39	54.9	427	4	US-09-248-796A-17203	Sequence 17203, A
30	38	53.5	15	4	US-09-053-611-33	Sequence 33, Appl
31	37	52.1	67	4	US-09-248-796A-24749	Sequence 24749, A
32	37	52.1	226	4	US-09-248-796A-19244	Sequence 19244, A
33	37	52.1	232	4	US-09-248-796A-16863	Sequence 16863, A
34	37	52.1	283	4	US-09-602-777A-20	Sequence 20, Appl
35	37	52.1	367	4	US-09-270-767-39016	Sequence 39016, A
36	37	52.1	367	4	US-09-270-767-54233	Sequence 54233, A
37	37	52.1	601	4	US-09-902-540-11184	Sequence 11184, A
38	37	52.1	2781	4	US-09-698-295-10	Sequence 10, Appl
39	37	52.1	2907	4	US-09-698-295-1	Sequence 1, Appli
40	36.5	51.4	114	4	US-09-248-796A-20576	Sequence 20576, A
41	36	50.7	303	4	US-09-248-796A-20412	Sequence 20412, A
42	36	50.7	316	4	US-09-543-681A-4590	Sequence 4590, Ap
43	36	50.7	379	4	US-09-134-000C-4846	Sequence 4846, Ap
44	36	50.7	495	4	US-09-252-991A-20739	Sequence 20739, A
45	36	50.7	505	4	US-09-949-016-6704	Sequence 6704, Ap

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:16:10 ; Search time 11.1587 Seconds
(without alignments)
484.703 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	71	100.0	19	15	US-10-346-162-242	Sequence 242, App
2	71	100.0	20	15	US-10-414-692-52	Sequence 52, Appl
3	71	100.0	20	15	US-10-414-583-10	Sequence 10, Appl
4	71	100.0	25	9	US-09-821-984-29	Sequence 29, Appl
5	71	100.0	25	15	US-10-637-190-3	Sequence 3, Appli
6	71	100.0	31	9	US-09-281-717-7	Sequence 7, Appli
7	71	100.0	31	9	US-09-281-717-10	Sequence 10, Appl
8	71	100.0	31	9	US-09-281-717-13	Sequence 13, Appl
9	71	100.0	1263	14	US-10-170-682-1	Sequence 1, Appli
10	71	100.0	1263	14	US-10-217-141-3	Sequence 3, Appli

11	71	100.0	1263	14	US-10-185-731-3	Sequence 3, Appli
12	71	100.0	1263	14	US-10-185-721-3	Sequence 3, Appli
13	71	100.0	1464	9	US-09-842-256-2	Sequence 2, Appli
14	61	85.9	20	15	US-10-414-583-52	Sequence 52, Appl
15	59	83.1	20	15	US-10-414-692-55	Sequence 55, Appl
16	59	83.1	20	15	US-10-414-583-13	Sequence 13, Appl
17	59	83.1	22	9	US-09-815-156-10	Sequence 10, Appl
18	59	83.1	25	9	US-09-821-984-28	Sequence 28, Appl
19	59	83.1	25	15	US-10-637-190-2	Sequence 2, Appli
20	59	83.1	32	9	US-09-281-717-16	Sequence 16, Appl
21	59	83.1	32	9	US-09-281-717-19	Sequence 19, Appl
22	59	83.1	32	9	US-09-281-717-22	Sequence 22, Appl
23	59	83.1	149	9	US-09-864-761-37262	Sequence 37262, A
24	59	83.1	951	14	US-10-379-616-8	Sequence 8, Appli
25	59	83.1	951	16	US-10-473-127-354	Sequence 354, App
26	59	83.1	1402	14	US-10-379-616-12	Sequence 12, Appl
27	59	83.1	1412	16	US-10-473-127-351	Sequence 351, App
28	59	83.1	1412	16	US-10-473-127-352	Sequence 352, App
29	59	83.1	1412	16	US-10-473-127-356	Sequence 356, App
30	59	83.1	1412	16	US-10-473-127-357	Sequence 357, App
31	59	83.1	1415	16	US-10-408-765A-2282	Sequence 2282, Ap
32	59	83.1	1417	16	US-10-473-127-348	Sequence 348, App
33	59	83.1	1417	16	US-10-473-127-359	Sequence 359, App
34	59	83.1	1420	14	US-10-379-616-4	Sequence 4, Appli
35	59	83.1	1420	16	US-10-473-127-349	Sequence 349, App
36	59	83.1	1420	16	US-10-473-127-353	Sequence 353, App
37	59	83.1	1420	16	US-10-473-127-358	Sequence 358, App
38	59	83.1	1424	15	US-10-418-027-1	Sequence 1, Appli
39	59	83.1	1424	16	US-10-473-127-347	Sequence 347, App
40	59	83.1	1424	16	US-10-473-127-350	Sequence 350, App
41	59	83.1	1424	16	US-10-473-127-360	Sequence 360, App
42	59	83.1	1438	16	US-10-333-894A-19	Sequence 19, Appl
43	59	83.1	1522	16	US-10-473-127-355	Sequence 355, App
44	58	81.7	48	9	US-09-842-256-5	Sequence 5, Appli
45	54	76.1	14	9	US-09-953-031A-4	Sequence 4, Appli

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:08:54 ; Search time 2.4797 Seconds
(without alignments)
543.224 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	71	100.0	1462	2	T42639	glucocorticoid rec
2	71	100.0	1463	2	T30193	nuclear receptor c
3	59	83.1	1424	2	T03851	thyroid hormone re
4	54	76.1	1061	2	A57620	steroid receptor c
5	43	60.6	229	2	D82230	hypothetical prote
6	42	59.2	99	2	S32700	hypothetical prote
7	42	59.2	261	2	S14882	hypothetical prote
8	42	59.2	342	2	AF2177	glucokinase [impor
9	42	59.2	369	2	T35306	hypothetical prote
10	42	59.2	474	2	T23547	hypothetical prote
11	41	57.7	407	2	H81289	probable sugar tra
12	41	57.7	2262	2	S16664	large protein L -
13	40	56.3	372	2	A64462	8-amino-7-oxononan
14	40	56.3	889	2	T09055	protocadherin 68 -
15	40	56.3	2269	1	JQ1750	genome polyprotein
16	39	54.9	167	2	S73043	hypothetical prote
17	39	54.9	216	2	F90393	phosphoglycerate m
18	39	54.9	364	1	A64729	3-isopropylmalate
19	39	54.9	364	2	E85489	3-isopropylmalate
20	39	54.9	364	2	E90638	3-isopropylmalate
21	39	54.9	389	2	E72761	hypothetical prote
22	39	54.9	420	2	F70842	hypothetical prote
23	39	54.9	423	2	H86996	conserved hypothet
24	39	54.9	582	2	S24545	intermediate filam
25	39	54.9	826	2	F64746	probable membrane
26	39	54.9	2255	1	JQ1532	genome polyprotein
27	38	53.5	218	2	A46143	mu-class glutathio
28	38	53.5	218	2	A23732	glutathione transf

29	38	53.5	268	2	AB1424	E. coli RpiR trans
30	38	53.5	268	2	AH1797	E. coli RpiR trans
31	38	53.5	284	2	AD1141	hypothetical prote
32	38	53.5	284	2	AG1499	hypothetical prote
33	38	53.5	377	2	T40024	probable cytochrom
34	38	53.5	378	2	T18486	hypothetical prote
35	38	53.5	395	2	D87678	thiolase family pr
36	38	53.5	503	2	T51156	calcium dependent
37	38	53.5	546	2	T04336	glutathione syntha
38	38	53.5	623	2	A70741	hypothetical prote
39	38	53.5	841	2	D84513	probable retroelem
40	38	53.5	851	2	H84053	endo-beta-1,3-1,4
41	38	53.5	927	2	T00357	hypothetical prote
42	38	53.5	6359	2	T31679	bacitracin synthet
43	37	52.1	103	2	G42528	B26R protein - vac
44	37	52.1	125	2	B97280	hypothetical prote
45	37	52.1	244	2	T22779	hypothetical prote

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:07:23 ; Search time 11.572 Seconds
(without alignments)
619.524 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	71	100.0	873	2 Q8BN74	Q8bn74 mus musculu
2	71	100.0	1393	2 Q7TPU7	Q7tpu7 mus musculu
3	71	100.0	1462	1 NCO2_MOUSE	Q61026 mus musculu
4	71	100.0	1464	1 NCO2_HUMAN	Q15596 homo sapien
5	71	100.0	1465	1 NCO2_RAT	Q9wui9 rattus norv
6	68	95.8	1505	2 Q98TW1	Q98tw1 brachydanio
7	66	93.0	1516	1 NCO2_XENLA	Q9w705 xenopus lae
8	59	83.1	1082	1 NCO3_RAT	Q9epu2 rattus norv
9	59	83.1	1398	1 NCO3_MOUSE	O09000 m nuclear r
10	59	83.1	1424	1 NCO3_HUMAN	Q9y6q9 h nuclear r
11	57	80.3	1391	1 NCO3_XENLA	O57539 xenopus lae
12	54	76.1	1330	2 Q66JL7	Q66jl7 mus musculu
13	54	76.1	1441	1 NCO1_HUMAN	Q15788 homo sapien
14	54	76.1	1447	1 NCO1_MOUSE	P70365 mus musculu
15	54	76.1	1508	2 Q8UVH3	Q8uvh3 coturnix co
16	51	71.8	700	2 Q6N6F5	Q6n6f5 rhodopseudo
17	46	64.8	2271	2 Q8JVA6	Q8jva6 tioman viru
18	44	62.0	262	2 Q8CPF5	Q8cpf5 staphylococ
19	44	62.0	1576	2 Q8II47	Q8ii47 plasmodium
20	43	60.6	229	2 Q9KSR0	Q9ksr0 vibrio chol
21	43	60.6	262	2 Q73FL8	Q73fl8 wolbachia p
22	43	60.6	1538	2 Q7QAG9	Q7qag9 anopheles g
23	42.5	59.9	714	2 Q9LT80	Q9lt80 arabidopsis
24	42	59.2	261	2 Q04319	Q04319 pichia angu
25	42	59.2	342	1 GLK_ANASP	P58616 anabaena sp
26	42	59.2	369	2 Q9S2P6	Q9s2p6 streptomyce
27	42	59.2	474	2 Q93879	Q93879 caenorhabdi
28	42	59.2	609	1 DAK_PICAN	O60017 pichia angu
29	42	59.2	612	2 Q9C2P6	Q9c2p6 neurospora
30	41	57.7	138	2 Q9T237	Q9t237 phytophthor

31	41	57.7	287	2	Q6L091	Q6l091	microphilus
32	41	57.7	407	2	Q9PML7	Q9pml7	campylobact
33	41	57.7	687	2	Q7RB96	Q7rb96	plasmodium
34	41	57.7	1590	2	Q6BJE1	Q6bjel	debaryomyce
35	41	57.7	2262	1	RRPL_PI2HT	P26676	human parai
36	40.5	57.0	1877	2	Q6CFU4	Q6cfu4	yarrowia li
37	40	56.3	138	2	Q8N2Z9	Q8n2z9	homo sapien
38	40	56.3	163	2	Q8G4I3	Q8g4i3	bifidobacte
39	40	56.3	184	2	Q7MRQ5	Q7mrq5	wolinella s
40	40	56.3	208	2	Q6C2P1	Q6c2p1	yarrowia li
41	40	56.3	372	1	BIOF_METJA	Q58694	methanococc
42	40	56.3	526	2	Q6JPG3	Q6jpg3	neodiprion
43	40	56.3	709	2	Q8R5Z4	Q8r5z4	fusobacteri
44	40	56.3	761	2	O76733	O76733	drosophila
45	40	56.3	889	1	PC17_HUMAN	O14917	homo sapien